

OIPF

RAW SEQUENCE LISTING
 PATENT APPLICATION US/99/613,355

DATE: 07/25/2000
 TIME: 11:11:11

Input File: A:\Lippsseq
 Output File: N:\CRF3\07252000\1613355.raw

SEQUENCE LISTING

(i) GENERAL INFORMATION
 C--> 3 (1) APPLICANT: BINIE V. LIPPS AND FREDERICK W. LIPPS
 4 (2) TITLE OF INVENTION: SYNTHETIC PEPTIDE FOR
 5 NEUROLOGICAL DISORDERS
 6 (3) NUMBER OF SEQUENCES: 1
 7 (4) THE SEQUENCE ADDRESS:
 8 (A) ADDRESS: JOHN R. WYSPEN
 9 (B) ADDRESS: PO BOX 1104
 10 (C) CITY: FRIENDSWOOD
 11 (D) STATE: TEXAS
 12 (E) COUNTRY: USA
 13 (F) ZIP: 77519
 14 (5) COMPUTER READABLE FORM:
 15 (A) MEDIUM TYPE: 3.5" FLOPPY DISK 1.44 MB
 16 (B) COMPUTER: IBM COMP-1.002
 17 (C) OPERATING SYSTEM: MS DOS 7.1/ WINDOWS 95
 18 (D) SOFTWARE: MICROSOFT 3.1 FOR WINDOWS
 C--> 19 (vi) CURRENT APPLICATION DATA:
 C--> 20 (A) APPLICATION NUMBER: US/69/613,355
 C--> 21 (B) FILING DATE: 11-Jul-2000
 22 (C) CLASSIFICATION: PRELIMINARY CLASS
 C--> 27 (viii) ATTORNEY/AGENT INFORMATION:
 28 (A) NAME: JOHN R. WYSPEN
 29 (B) REGISTRATION NUMBER: 19 108
 30 (C) REFERENCE/DOCKET NUMBER: 1613355.13
 C--> 0 (ix) TELECOMMUNICATION INFORMATION:
 31 (A) TELEPHONE: 281-460-7961
 32 (B) TELEFAX: 281-461-8402
 33 (C) TELEX:

Does Not Comply
 Correct Format Needed

Suggestion

*Consult
 Sequence Rules
 for valid
 format*

ERRORED SEQUENCES

34 (1) INFORMATION FOR SEQ ID NO: 1
 35 (1) SEQUENCE CHARACTERISTICS:
 36 (A) LENGTH: 116
 37 (B) TYPE: AMINO ACID
 38 (C) STRANDEDNESS: SINGLE
 39 (D) TOPOLOGY: LINEAR
 40 (1) MOLECULE TYPE: PROTEIN IN SEQ ID NO: 1
 41 (11) HYPOTHEICAL: NO
 42 (12) ANTI-SENSE:
 W--> 40 (v) FRAGMENT TYPE:
 41 (12) ORIGINAL SOURCE:
 42 (A) ORGANISM: HOMO SAPIENS
 43 (B) STRAIN: WILD

RAW SEQUENCE LISTING
 (1) NAME: CRF3 Vsr1613355

DATE: 10/2/95
 TIME: 11:00

Input File: AnLippseq
 Output File: \CRF3\17252000\1613355.raw

11 (1) INDIVIDUAL ISOLATE
 12 (2) DEVELOPMENTAL STAGE: ADULT
 13 (3) HEMISPHERE
 14 (4) TISSUE TYPE
 15 (5) CELL TYPE
 16 (6) CELL LINE
 17 (I) ORGANELLE:
 C--> 50
 C--> 52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 53 ~~Met~~
 E--> 55 ~~Glu~~AspHisProValHisAsnIleuGlyGluHisProValCysAsx
 E--> 56 SerThrAshThrTrp20ValGlyValLysThrThrAlaThrAsnIle
 E--> 57 LysGlyAlaSerValSerValMetGluAsx40ValAsnLeuAspAsn
 58 ~~Leu~~ValTyrIleGlnIlePhePheGluIleAsxThrGlxHisIrp
 E--> 59 AsxProProGlxProGlyCysLysGlyIleAsxThrGlxHisIrp
 E--> 60 AsxSerTyrCysThr80ThrSerAsnSerPheIleLysAlaLeuThr
 F--> 61 MetAsxGlxGlyGlnSerAlaTrpArgPhe100IleArgIleGlxThr
 E--> 62 AlaCysValCysValIleThrLysLysGlyAsn
 E--> 63 COOH
 C--> 65 (2) INFORMATION FOR SEQ ID NO: 1:
 66 (i) SEQUENCE CHARACTERISTICS:
 67 (A) LENGTH: 10
 68 (B) TYPE: AMINO ACID
 69 (C) STRANDEDNESS: SINGLE
 70 (D) TOPOLOGY: LINEAR
 71 (ii) MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 1
 72 (iii) HYPOTHETICAL: NO
 73 (iv) ANTI-SENSE:
 W--> 74 (v) FRAGMENT TYPE:
 75 (vi) ORIGINAL SOURCE:
 76 (A) ORGANISM:
 77 (B) STRAIN:
 78 (C) INDIVIDUAL ISOLATE
 79 (D) DEVELOPMENTAL STAGE:
 80 (E) HEMISPHERE:
 81 (F) TISSUE TYPE:
 82 (G) CELL TYPE:
 83 (H) CELL LINE:
 84 (I) ORGANELLE:
 C--> 84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 C--> 86 N L G E H P V C D S I D I W V
 E--> 87
 C--> 88 (2) INFORMATION FOR SEQ ID NO: 3:
 89 (i) SEQUENCE CHARACTERISTICS:
 90 (A) LENGTH: 10
 91 (B) TYPE: AMINO ACID
 92 (C) STRANDEDNESS: SINGLE
 93 (D) TOPOLOGY: LINEAR
 94 (ii) MOLECULE TYPE: PEPTIDE IN SEQ ID NO: 3
 95 (iii) HYPOTHETICAL: NO
 96 (iv) ANTI-SENSE:

invalid

delete

invalid

For 1.822 of
 Sequence Rules,
 do not show
 amino or
 Carboxy groups

1) delete all
 dashes;

2) Number the
 amino acids
 under every 5
 amino acids -
 do not use
 TAB codes,
 between amino
 acid nos.

Per Sequence Rules,
 use three-letter
 amino acids

Input: Port: A:\Lippeseq
Output: Port: N:\CRF3\07252000\1613355.raw

W--> 97 (v) FRAGMENT TYPE:
 (1) ORIGINAL SOURCE:
 (2) ORGANISM:
 (3) STRAIN:
 (4) INDIVIDUAL ISOLATE:
 (5) DEVELOPMENTAL STAGE:
 (6) HOST TYPE:
 (7) TISSUE TYPE:
 (8) CELL TYPE:
 (9) CELL LINE:
 (1) ORGANEILE:
 C--> 107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 C--> 109 N L G E H P V C D S
 E--> 110
 C--> 112 (2) INFORMATION FOR SEQ ID NO: 4:
 (1) SEQUENCE CHARACTERISTICS:
 (a) LENGTH:
 (b) TYPE: NUCLEIC ACID
 (c) STRANDEDNESS: SINGLE
 (d) TOPOLOGY: LINEAR
 (11) MAPLETYPE: PHOSPHORIC ACID
 (111) HYDROLYTIC: NO
 (112) ANTI-SENSE:
 (v) FRAGMENT TYPE:
 (1) ORIGINAL SOURCE:
 (2) ORGANISM:
 (3) STRAIN:
 (4) INDIVIDUAL ISOLATE:
 (5) DEVELOPMENTAL STAGE:
 (6) HOST TYPE:
 (7) TISSUE TYPE:
 (8) CELL TYPE:
 (9) CELL LINE:
 (1) ORGANEILE:
 C--> 131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 C--> 133 N L G E H
 E--> 134

Same error

(X1) SEQUENCE
NLGEH → same

